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<110> Nezu, Jun-Ichi
Oku, Asuka

<120> TRANSPORTER GENES

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<141> 2000-03-07

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Trp Glu Met Phe Thr Val Leu Phe Val Ile Val Gly Met Gly Gln Ile
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<210> 9
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<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 9
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<210> 10
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<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 10
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<210> 11
 <211> 22
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<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 11
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<210> 12
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<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 12

tcacacagga aacagctatg ac

22

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 13

gtgctgttg gctccttcat ttca

24

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 14

agctgcatga agagaaggac actg

24

<210> 15

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

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agcatcctgt ctccctactt cggt

24

<210> 16

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 16

gatggatccc ggacggtctt gggtcgcctg ctg

33

<210> 17

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 17

gatggatcca aatgctgcca catagttgga gat 33

<210> 18

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 18

gatggatcca tgggcatgca gacaggcttc agc 33

<210> 19

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 19

gatggatcct tcctcttcag tttctccctt act 33

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 20

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<210> 21

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 21

aggcttttga tttgttctgt tgag 24

<210> 22

<211> 553

<212> PRT

<213> Mus musculus

<400> 22

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 1           5           10           15

Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
          20           25           30

Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His
          35           40           45

Arg Cys Leu Val Pro Asp Thr Val Asn Leu Ser Ser Ser Trp Arg Asn
          50           55           60

His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Ser
          65           70           75           80

Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Met Gly
          85           90           95

Leu Glu Pro Gly Gln Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
          100          105          110

Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Ile Phe Leu Ser Thr Ile
          115          120          125

Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Thr Pro Leu
          130          135          140

Thr Thr Ser Leu Phe Phe Val Gly Val Leu Cys Gly Ser Phe Val Ser
          145          150          155          160

Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Lys Val Leu Phe Ala Thr
          165          170          175

Met Ala Val Gln Thr Gly Phe Ser Phe Val Gln Ile Phe Ser Thr Asn
          180          185          190

Trp Glu Met Phe Thr Val Leu Phe Ala Ile Val Gly Met Gly Gln Ile
          195          200          205

Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Ser Lys
          210          215          220

Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala
          225          230          235          240

Ile Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
          245          250          255

Arg Met Leu Leu Leu Ala Leu Thr Leu Pro Gly Leu Phe Cys Val Pro
          260          265          270

Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
          275          280          285

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Arg Phe Ala Glu Ala Glu Gln Ile Ile Gln Lys Ala Ala Lys Met Asn
 290 295 300
 Ser Ile Val Ala Pro Ala Gly Ile Phe Asp Pro Leu Glu Leu Gln Glu
 305 310 315 320
 Leu Asn Ser Leu Lys Gln Gln Lys Val Ile Ile Leu Asp Leu Phe Arg
 325 330 335
 Thr Arg Asn Ile Ala Thr Ile Thr Val Met Ala Val Met Leu Trp Met
 340 345 350
 Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu Asn Val Pro Asn Leu
 355 360 365
 His Gly Asp Val Tyr Leu Asn Cys Phe Leu Ser Gly Leu Ile Glu Val
 370 375 380
 Pro Ala Tyr Phe Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg
 385 390 395 400
 Tyr Ile Ile Ala Gly Val Leu Phe Trp Gly Gly Gly Val Leu Leu Leu
 405 410 415
 Ile Gln Val Val Pro Glu Asp Tyr Asn Phe Val Ser Ile Gly Leu Val
 420 425 430
 Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val
 435 440 445
 Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly
 450 455 460
 Ile Thr Ser Met Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe
 465 470 475 480
 Val Tyr Leu Gly Ala Tyr Asn Arg Leu Leu Pro Tyr Ile Leu Met Gly
 485 490 495
 Ser Leu Thr Val Leu Ile Gly Ile Ile Thr Leu Phe Phe Pro Glu Ser
 500 505 510
 Phe Gly Val Thr Leu Pro Glu Asn Leu Glu Gln Met Gln Lys Val Arg
 515 520 525
 Gly Phe Arg Cys Gly Lys Lys Ser Thr Val Ser Val Asp Arg Glu Glu
 530 535 540
 Ser Pro Lys Val Leu Ile Thr Ala Phe
 545 550

<210> 23

<211> 2083

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (122)..(1780)

<400> 23

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tcgctgaatc ctttctctcc acccacctcc ctcacgcaag ctgaggagga gaggtggaaa      120

c atg cgg gac tac gac gag gtg atc gcc ttc ctg ggc gag tgg ggg ccc      169
  Met Arg Asp Tyr Asp Glu Val Ile Ala Phe Leu Gly Glu Trp Gly Pro
    1         5         10        15
ttc cag cgc ctc atc ttc ttt ctg ctc agc gcc agc atc atc ccc aat      217
Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
    20        25        30
ggc ttc aat ggt atg tca gtc gtg ttc ctg gcg ggg acc ccc gag cac      265
Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His
    35        40        45
cgt tgc ctg gtt cct gac act gtg aac ctg agc agc tcc tgg cgc aac      313
Arg Cys Leu Val Pro Asp Thr Val Asn Leu Ser Ser Ser Trp Arg Asn
    50        55        60
cac agc atc ccc ttg gag acg aag gac gga cga cag gtg cct cag agc      361
His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Ser
    65        70        75        80
tgc cgc cgc tac cga ctg gcc acc atc gcc aac ttc tct gcg atg ggg      409
Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Met Gly
    85        90        95
ctg gag cca gga cag gac gtg gat ctg gag cag ctg gag cag gag agc      457
Leu Glu Pro Gly Gln Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
    100       105       110
tgc ctg gat ggc tgg gag tac gac aag gac atc ttc ctg tcc acc atc      505
Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Ile Phe Leu Ser Thr Ile
    115       120       125
gtg aca gag tgg aat ctg gtg tgt gag gat gac tgg aag aca ccc ctc      553
Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Thr Pro Leu
    130       135       140
acc acc tcc ctg ttc ttc gta ggc gtt ctc tgc ggc tcc ttc gtg tct      601
Thr Thr Ser Leu Phe Phe Val Gly Val Leu Cys Gly Ser Phe Val Ser
    145       150       155       160
ggg cag ctg tca gac agg ttt ggc agg aag aaa gtc ctc ttt gca acc      649
Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Lys Val Leu Phe Ala Thr
    165       170       175
atg gct gtg cag act gga ttc agc ttc gtg cag att ttc tca acc aac      697
Met Ala Val Gln Thr Gly Phe Ser Phe Val Gln Ile Phe Ser Thr Asn
    180       185       190
tgg gag atg ttc act gtg ttg ttt gcc att gtg ggc atg ggc cag atc      745

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Trp	Glu	Met	Phe	Thr	Val	Leu	Phe	Ala	Ile	Val	Gly	Met	Gly	Gln	Ile		
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tcc	aac	tac	gtg	gtg	gcc	ttc	ata	cta	gga	act	gaa	atc	ctg	agc	aag	793	
Ser	Asn	Tyr	Val	Val	Ala	Phe	Ile	Leu	Gly	Thr	Glu	Ile	Leu	Ser	Lys		
	210					215					220						
tcg	gtt	cgc	atc	atc	ttc	tcc	aca	tta	gga	gtc	tgt	aca	ttt	ttt	gca	841	
Ser	Val	Arg	Ile	Ile	Phe	Ser	Thr	Leu	Gly	Val	Cys	Thr	Phe	Phe	Ala		
225					230					235					240		
atc	ggc	tac	atg	gtc	ctg	ccg	ctg	ttt	gca	tac	ttc	atc	aga	gac	tgg	889	
Ile	Gly	Tyr	Met	Val	Leu	Pro	Leu	Phe	Ala	Tyr	Phe	Ile	Arg	Asp	Trp		
				245					250					255			
agg	atg	ctg	ctg	ctg	gcc	ctg	aca	ctg	cct	ggc	ctg	ttc	tgt	gtt	ccc	937	
Arg	Met	Leu	Leu	Leu	Ala	Leu	Thr	Leu	Pro	Gly	Leu	Phe	Cys	Val	Pro		
			260					265					270				
ctg	tgg	tgg	ttt	att	cca	gaa	tct	ccc	cgg	tgg	ctg	ata	tcc	cag	agg	985	
Leu	Trp	Trp	Phe	Ile	Pro	Glu	Ser	Pro	Arg	Trp	Leu	Ile	Ser	Gln	Arg		
		275					280					285					
aga	ttt	gca	gag	gcc	gaa	cag	atc	atc	cag	aaa	gcc	gca	aag	atg	aac	1033	
Arg	Phe	Ala	Glu	Ala	Glu	Gln	Ile	Ile	Gln	Lys	Ala	Ala	Lys	Met	Asn		
	290					295					300						
agc	atc	gtg	gcg	cca	gca	ggg	ata	ttc	gat	cct	cta	gag	cta	cag	gag	1081	
Ser	Ile	Val	Ala	Pro	Ala	Gly	Ile	Phe	Asp	Pro	Leu	Glu	Leu	Gln	Glu		
305					310					315					320		
cta	aac	tcc	ttg	aag	cag	cag	aaa	gtc	ata	atc	ctg	gac	ctg	ttc	agg	1129	
Leu	Asn	Ser	Leu	Lys	Gln	Gln	Lys	Val	Ile	Ile	Leu	Asp	Leu	Phe	Arg		
				325				330						335			
act	cgg	aac	att	gcc	acc	ata	acc	gtg	atg	gct	gtg	atg	ctg	tgg	atg	1177	
Thr	Arg	Asn	Ile	Ala	Thr	Ile	Thr	Val	Met	Ala	Val	Met	Leu	Trp	Met		
			340					345					350				
cta	acc	tca	gtg	ggt	tac	ttt	gct	ctg	tct	ctc	aat	gtt	cct	aat	tta	1225	
Leu	Thr	Ser	Val	Gly	Tyr	Phe	Ala	Leu	Ser	Leu	Asn	Val	Pro	Asn	Leu		
		355					360					365					
cat	gga	gat	gtc	tac	ctg	aac	tgc	ttc	ctc	tct	ggc	ctg	att	gaa	gtt	1273	
His	Gly	Asp	Val	Tyr	Leu	Asn	Cys	Phe	Leu	Ser	Gly	Leu	Ile	Glu	Val		
	370					375					380						
cca	gct	tac	ttc	aca	gcc	tgg	ctg	cta	ctg	cga	acc	ctg	cca	cgg	aga	1321	
Pro	Ala	Tyr	Phe	Thr	Ala	Trp	Leu	Leu	Leu	Arg	Thr	Leu	Pro	Arg	Arg		
385					390					395					400		
tat	att	ata	gct	ggg	gtg	cta	ttc	tgg	gga	gga	ggt	gtg	ctt	ctc	ttg	1369	
Tyr	Ile	Ile	Ala	Gly	Val	Leu	Phe	Trp	Gly	Gly	Gly	Val	Leu	Leu	Leu		
				405					410					415			
atc	caa	gtg	gta	cct	gaa	gat	tat	aac	ttt	gtg	tcc	att	gga	ctg	gtg	1417	
Ile	Gln	Val	Val	Pro	Glu	Asp	Tyr	Asn	Phe	Val	Ser	Ile	Gly	Leu	Val		

420	425	430	
atg ctg ggg aaa ttt ggg atc acc tct gcc ttc tcc atg ttg tat gtc			1465
Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val			
435	440	445	
ttc act gcg gag ctc tac cca acc ctg gtc agg aac atg gct gtg ggc			1513
Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly			
450	455	460	
atc acc tcc atg gcc tct cgg gtg ggc agc atc att gcc ccc tat ttc			1561
Ile Thr Ser Met Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe			
465	470	475	480
gtt tac ctg ggc gcc tat aac aga ctc cta ccc tac atc ctc atg ggc			1609
Val Tyr Leu Gly Ala Tyr Asn Arg Leu Leu Pro Tyr Ile Leu Met Gly			
485	490	495	
agt ctg act gtc ctc att gga atc atc acg ctt ttt ttc cct gaa agt			1657
Ser Leu Thr Val Leu Ile Gly Ile Ile Thr Leu Phe Phe Pro Glu Ser			
500	505	510	
ttt gga gtg act cta cca gag aac ttg gag cag atg cag aaa gtg aga			1705
Phe Gly Val Thr Leu Pro Glu Asn Leu Glu Gln Met Gln Lys Val Arg			
515	520	525	
ggg ttc aga tgt ggg aaa aaa tca aca gtc tca gtg gac aga gaa gaa			1753
Gly Phe Arg Cys Gly Lys Lys Ser Thr Val Ser Val Asp Arg Glu Glu			
530	535	540	
agc ccc aag gtt cta ata act gca ttc taacgagggtt tccaaggcac			1800
Ser Pro Lys Val Leu Ile Thr Ala Phe			
545	550		
ttggcaaact gaaaagcaga tgtatacaat gagcaggggtg tgatagagca agcctgcaat			1860
cccagcgctc ttgggggtgga gacagaagat caggagttca aggtcatcct tggctacagc			1920
aggagtgtaa gaccagcctg tcttaccaca agcaaccctg tctcaacaga acaaatcaaa			1980
agcctttttct gctgaaaggg attaacagaa acaatgagca ccaaactgga cttgtggaga			2040
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<210> 24			
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<400> 24			
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<211> 24
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 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 25
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<210> 26
 <211> 24
 <212> DNA
 <213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 26
 tgtttttcgt ggggtgtgctg atgg 24

<210> 27
 <211> 557
 <212> PRT
 <213> Mus musculus

<400> 27
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 Gly Phe Asn Gly Met Ser Ile Val Phe Leu Ala Gly Thr Pro Glu His
 35 40 45
 Arg Cys Leu Val Pro His Thr Val Asn Leu Ser Ser Ala Trp Arg Asn
 50 55 60
 His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Lys
 65 70 75 80
 Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Glu Leu Gly
 85 90 95
 Leu Glu Pro Gly Arg Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
 100 105 110
 Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Val Phe Leu Ser Thr Ile
 115 120 125
 Val Thr Glu Trp Asp Leu Val Cys Lys Asp Asp Trp Lys Ala Pro Leu
 130 135 140
 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Met Gly Ser Phe Ile Ser

145		150		155		160
Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Leu Thr						
		165		170		175
Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Val Phe Ser Val Asn						
		180		185		190
Phe Glu Met Phe Thr Val Leu Phe Val Leu Val Gly Met Gly Gln Ile						
		195		200		205
Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Ser Lys						
		210		215		220
Ser Ile Arg Ile Ile Phe Ala Thr Leu Gly Val Cys Ile Phe Tyr Ala						
		225		230		240
Phe Gly Phe Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp						
		245		250		255
Arg Met Leu Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Gly Ala						
		260		265		270
Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Gly						
		275		280		285
Arg Ile Lys Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ile Asn						
		290		295		300
Gly Ile Val Ala Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln Asp						
		305		310		320
Leu Asn Ser Thr Lys Pro Gln Leu His His Ile Tyr Asp Leu Ile Arg						
		325		330		335
Thr Arg Asn Ile Arg Val Ile Thr Ile Met Ser Ile Ile Leu Trp Leu						
		340		345		350
Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn Leu						
		355		360		365
His Gly Asp Ile Tyr Val Asn Cys Phe Leu Leu Ala Ala Val Glu Val						
		370		375		380
Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg Arg						
		385		390		400
Tyr Ser Ile Ser Ala Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe						
		405		410		415
Met Gln Leu Val Pro Ser Glu Leu Phe Tyr Leu Ser Thr Ala Leu Val						
		420		425		430
Met Val Gly Lys Phe Gly Ile Thr Ser Ala Tyr Ser Met Val Tyr Val						
		435		440		445
Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly						

450 455 460

Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr Phe
465 470 475 480

Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly
485 490 495

Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Phe Pro Glu Ser
500 505 510

Phe Gly Val Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys
515 520 525

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<220>
<221> CDS
<222> (60)..(1730)

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Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly Pro
1 5 10 15

ttc cag cgc ctc atc ttc ttc ctg ctc agc gcc agc atc atc ccc aat 155
Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
20 25 30

ggc ttc aat ggt atg tcc atc gtg ttc ctg gcg ggg acc ccg gag cac 203
Gly Phe Asn Gly Met Ser Ile Val Phe Leu Ala Gly Thr Pro Glu His
35 40 45

cgt tgc ctt gtg cct cac acc gtg aac ctg agc agc gcg tgg cgc aac 251
Arg Cys Leu Val Pro His Thr Val Asn Leu Ser Ser Ala Trp Arg Asn
50 55 60

cac agt atc ccg ttg gag acg aag gac gga cga cag gtg cct cag aaa 299
His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Lys
65 70 75 80

tgc cgc cgc tac cga ctg gcc acc atc gcc aac ttc tct gag cta ggg 347
Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Glu Leu Gly
85 90 95

ctg gag ccg ggg cgg gac gtg gac ctg gag cag ctg gag cag gag agc 395

Leu	Glu	Pro	Gly	Arg	Asp	Val	Asp	Leu	Glu	Gln	Leu	Glu	Gln	Glu	Ser		
			100					105					110				
tgc	ctg	gat	ggc	tgg	gag	tac	gac	aag	gac	gtc	ttc	ctg	tcc	acc	atc	443	
Cys	Leu	Asp	Gly	Trp	Glu	Tyr	Asp	Lys	Asp	Val	Phe	Leu	Ser	Thr	Ile		
		115					120					125					
gtg	aca	gag	tgg	gac	ctg	gtg	tgt	aag	gat	gac	tgg	aaa	gcc	cca	ctc	491	
Val	Thr	Glu	Trp	Asp	Leu	Val	Cys	Lys	Asp	Asp	Trp	Lys	Ala	Pro	Leu		
	130					135					140						
acc	acc	tcc	ttg	ttt	ttc	gtg	ggg	gtg	ctg	atg	ggc	tcc	ttc	att	tca	539	
Thr	Thr	Ser	Leu	Phe	Phe	Val	Gly	Val	Leu	Met	Gly	Ser	Phe	Ile	Ser		
145					150				155						160		
gga	cag	ctc	tca	gac	agg	ttt	ggg	cgc	aag	aat	gtg	ctg	ttt	ttg	acc	587	
Gly	Gln	Leu	Ser	Asp	Arg	Phe	Gly	Arg	Lys	Asn	Val	Leu	Phe	Leu	Thr		
				165				170						175			
atg	ggc	atg	cag	act	ggc	ttc	agc	ttc	ctg	cag	gtc	ttc	tct	gtg	aac	635	
Met	Gly	Met	Gln	Thr	Gly	Phe	Ser	Phe	Leu	Gln	Val	Phe	Ser	Val	Asn		
			180					185					190				
ttc	gag	atg	ttt	aca	gtg	ctt	ttt	gtc	ctt	gtt	ggc	atg	ggg	cag	atc	683	
Phe	Glu	Met	Phe	Thr	Val	Leu	Phe	Val	Leu	Val	Gly	Met	Gly	Gln	Ile		
	195					200						205					
tcc	aac	tac	gtg	gca	gca	ttt	gtc	ctg	gga	aca	gaa	att	ctt	tcc	aag	731	
Ser	Asn	Tyr	Val	Ala	Ala	Phe	Val	Leu	Gly	Thr	Glu	Ile	Leu	Ser	Lys		
	210					215					220						
tca	att	cga	att	ata	ttc	gcc	acc	tta	gga	gtt	tgc	ata	ttt	tat	gcg	779	
Ser	Ile	Arg	Ile	Ile	Phe	Ala	Thr	Leu	Gly	Val	Cys	Ile	Phe	Tyr	Ala		
225					230				235					240			
ttt	ggc	ttc	atg	gtg	ctg	cca	ctg	ttt	gca	tac	ttc	atc	aga	gac	tgg	827	
Phe	Gly	Phe	Met	Val	Leu	Pro	Leu	Phe	Ala	Tyr	Phe	Ile	Arg	Asp	Trp		
				245				250					255				
agg	atg	ctg	ctg	ctg	gcg	ctc	act	gtg	cca	ggg	gtg	cta	tgt	ggg	gct	875	
Arg	Met	Leu	Leu	Leu	Ala	Leu	Thr	Val	Pro	Gly	Val	Leu	Cys	Gly	Ala		
			260					265					270				
ctc	tgg	tgg	ttc	atc	cct	gag	tcc	cca	cga	tgg	ctc	atc	tct	caa	ggc	923	
Leu	Trp	Trp	Phe	Ile	Pro	Glu	Ser	Pro	Arg	Trp	Leu	Ile	Ser	Gln	Gly		
		275					280					285					
cga	att	aaa	gag	gca	gag	gtg	atc	atc	cgc	aaa	gct	gcc	aaa	atc	aat	971	
Arg	Ile	Lys	Glu	Ala	Glu	Val	Ile	Ile	Arg	Lys	Ala	Ala	Lys	Ile	Asn		
	290					295					300						
ggg	att	gtt	gca	cct	tcc	act	atc	ttc	gat	cca	agt	gag	tta	caa	gac	1019	
Gly	Ile	Val	Ala	Pro	Ser	Thr	Ile	Phe	Asp	Pro	Ser	Glu	Leu	Gln	Asp		
305					310				315				320				
tta	aat	tct	acg	aag	cct	cag	ttg	cac	cac	att	tat	gat	ctg	atc	cga	1067	
Leu	Asn	Ser	Thr	Lys	Pro	Gln	Leu	His	His	Ile	Tyr	Asp	Leu	Ile	Arg		

	325		330		335	
aca cgg aat atc agg gtc atc acc atc atg tct ata atc ctg tgg ctg						1115
Thr Arg Asn Ile Arg Val Ile Thr Ile Met Ser Ile Ile Leu Trp Leu						
	340		345		350	
acc ata tca gtg ggc tat ttt gga cta tct ctt gac act cct aac ttg						1163
Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn Leu						
	355		360		365	
cat ggg gac atc tat gtg aac tgc ttc cta ctg gcg gct gtt gaa gtc						1211
His Gly Asp Ile Tyr Val Asn Cys Phe Leu Leu Ala Ala Val Glu Val						
	370		375		380	
cca gcc tat gtg ctg gcc tgg ctg ttg ttg cag tac ttg ccc cgg cga						1259
Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg Arg						
	385		390		395	400
tat tct atc tcg gct gcc ctt ttc ctg ggt ggc agt gtc ctt ctc ttc						1307
Tyr Ser Ile Ser Ala Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe						
	405		410		415	
atg cag ctg gtg cct tca gaa ttg ttt tac ttg tcc act gcc ctg gtg						1355
Met Gln Leu Val Pro Ser Glu Leu Phe Tyr Leu Ser Thr Ala Leu Val						
	420		425		430	
atg gtg ggg aag ttt gga atc acc tct gcc tac tcc atg gtc tat gtg						1403
Met Val Gly Lys Phe Gly Ile Thr Ser Ala Tyr Ser Met Val Tyr Val						
	435		440		445	
tac aca gct gag ctg tac ccc act gtg gtc aga aac atg ggt gtg ggg						1451
Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly						
	450		455		460	
gtc agc tcc aca gca tcc cgc ctt ggc agc atc ctg tct ccc tac ttt						1499
Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr Phe						
	465		470		475	480
gtt tac cta ggt gcc tat gat cgc ttc ctg cct tat att ctc atg gga						1547
Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly						
	485		490		495	
agt ctg acc atc ctg aca gct atc ctc acc ttg ttc ttc cct gag agc						1595
Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Phe Pro Glu Ser						
	500		505		510	
ttt ggt gtc cct ctc cca gat acc att gac cag atg cta agg gtc aaa						1643
Phe Gly Val Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys						
	515		520		525	
gga ata aaa cag tgg caa atc caa agc cag aca aga atg caa aaa gat						1691
Gly Ile Lys Gln Trp Gln Ile Gln Ser Gln Thr Arg Met Gln Lys Asp						
	530		535		540	
ggt gaa gaa agc cca aca gtc cta aag agc aca gcc ttc taacaccctg						1740
Gly Glu Glu Ser Pro Thr Val Leu Lys Ser Thr Ala Phe						
	545		550		555	

tccagaaggc aaaaaactga ttggaaacct tcatgttgtc agaaatgctc tccatgactg 1800
 agggccttttc tggtctgtta accttggtgc taacatgctc atggattggg gcatctgtcc 1860
 tggagagtca ccttcctcta gggacacc 1888

<210> 29
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 29
 ctaatacgac tcaactatagg gctcgagcgg ccgcccgggc aggt 44

<210> 30
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 30
 tgtagcgtga agacgacaga aagggcgtgg tgcggagggc ggt 43

<210> 31
 <211> 10
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 31
 acctgcccgg 10

<210> 32
 <211> 11
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 32
 accgccctcc g 11

<210> 33
 <211> 14

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Exemplary motif

<221> VARIANT
 <222> 1
 <223> Xaa = Leu, Ile, Val, Met, Ser, Thr, Ala, or Gly

<221> VARIANT
 <222> 2
 <223> Xaa = Leu, Ile, Val, Met, Phe, Ser, Ala, or Gly

<221> VARIANT
 <222> 3, 6, 11-13
 <223> Xaa = any amino acid

<221> VARIANT
 <222> 4
 <223> Xaa = Leu, Ile, Val, Met, Ser, or Ala

<221> VARIANT
 <222> 5
 <223> Xaa = Asp, or Glu

<221> VARIANT
 <222> 7
 <223> Xaa = Leu, Ile, Val, Met, Phe, Tyr, Trp, or Ala

<221> VARIANT
 <222> 10
 <223> Xaa = Arg, or Lys

<221> VARIANT
 <222> 14
 <223> Xaa = Gly, Ser, Thr, or Ala

<400> 33
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Arg Xaa Xaa Xaa Xaa Xaa
 1 5 10